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ATGGACAAAAC TCACACATGTCCACCTTGTCCAGCTCCGGAAC TCCTGGGGGGACCGTCA  
1 -----+-----+-----+-----+-----+ 60  
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTC  
61 -----+-----+-----+-----+-----+ 120  
CAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGGACTCCAG

a V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG  
121 -----+-----+-----+-----+-----+ 180  
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG  
181 -----+-----+-----+-----+-----+ 240  
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC  
241 -----+-----+-----+-----+-----+ 300  
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTTCCTCATG

a Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCC  
301 -----+-----+-----+-----+-----+ 360  
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTGGTAGAGGTTTCGG

a K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACC  
361 -----+-----+-----+-----+-----+ 420  
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG

a K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG  
421 -----+-----+-----+-----+-----+ 480  
TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAAC TACAAGACCACGCCTCCCGTGTGGAC  
481 -----+-----+-----+-----+-----+ 540  
CTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG

FIG. 1A

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a     E W E S N G Q P E N N Y K T T P P V L D     -  
  
TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG  
541     -----+-----+-----+-----+-----+-----+ 600  
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC  
  
a     S D G S F F L Y S K L T V D K S R W Q Q     -  
  
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG  
601     -----+-----+-----+-----+-----+-----+ 660  
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC  
  
a     G N V F S C S V M H E A L H N H Y T Q K     -  
  
AGCCTCTCCCTGTCTCCGGGTAAA  
661     -----+-----+-----+-----+-----+-----+ 684  
TCGGAGAGGGACAGAGGCCCATTT  
  
a     S L S L S P G K

FIG. 1B

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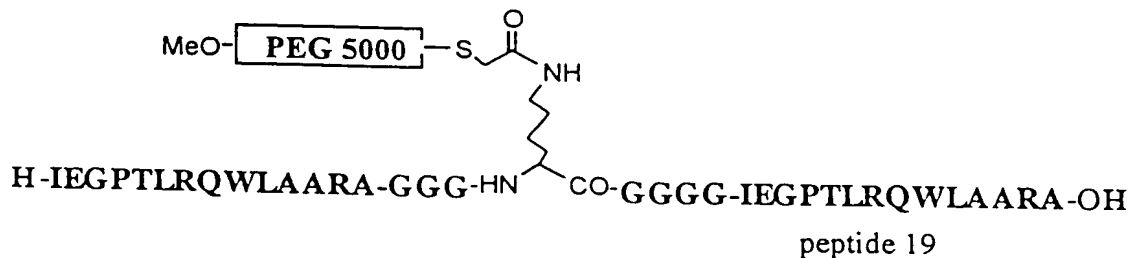
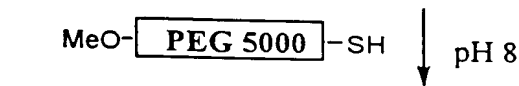
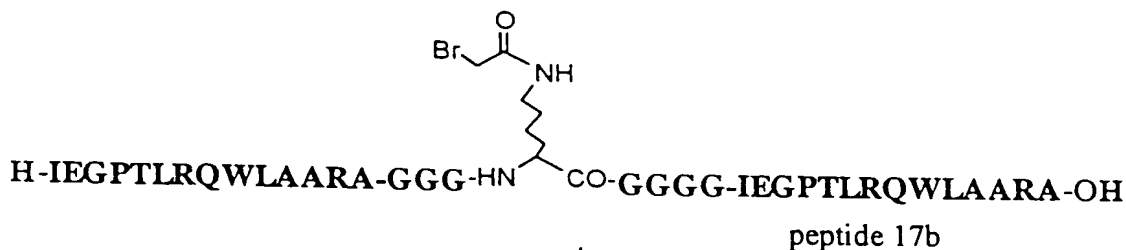
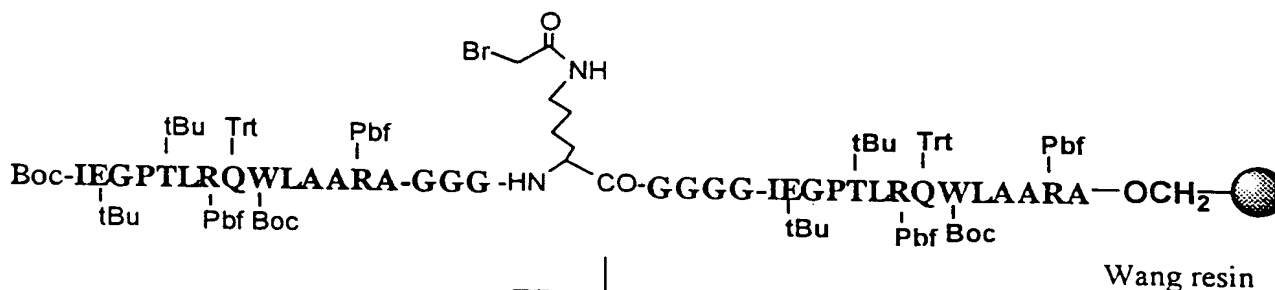
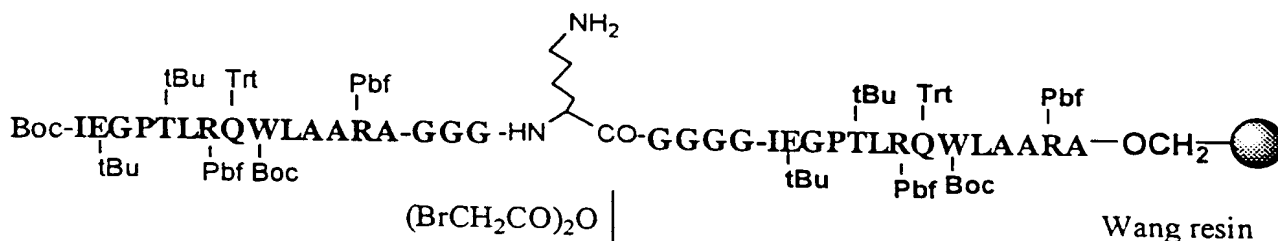
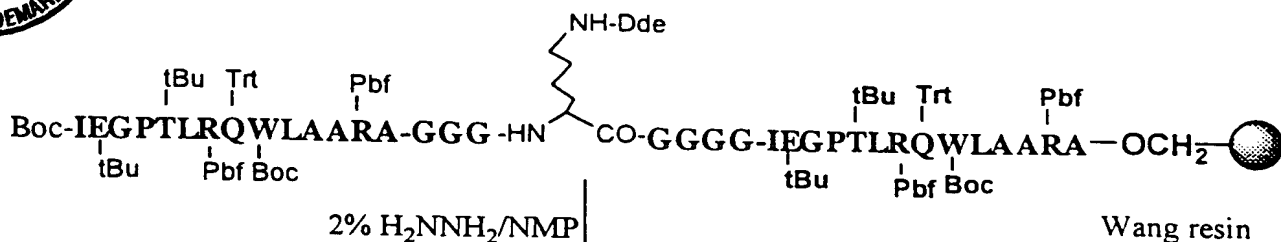


FIG. 2



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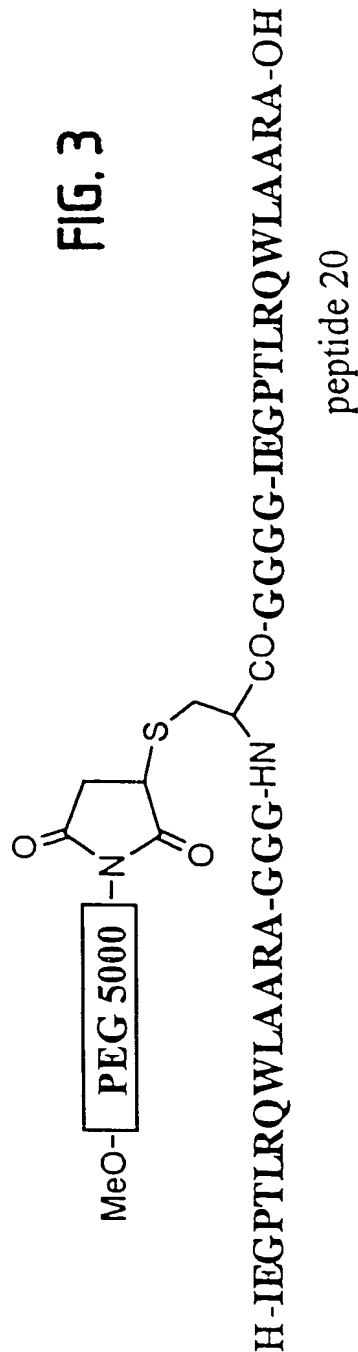
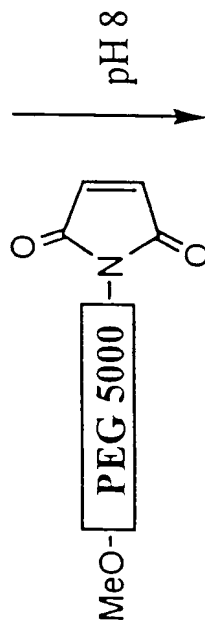
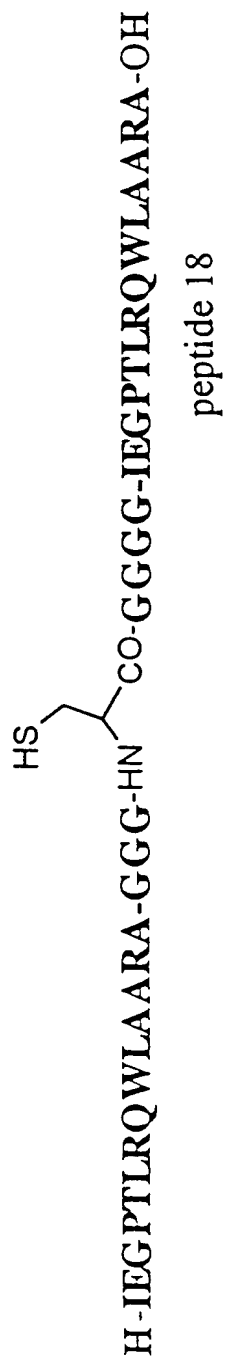
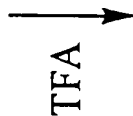
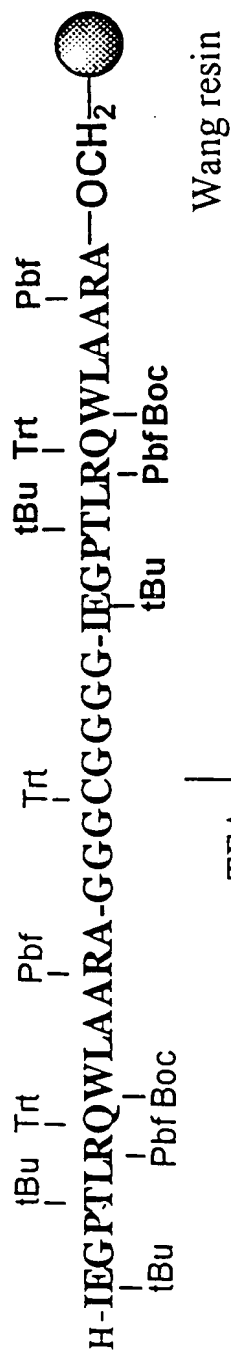


FIG. 3

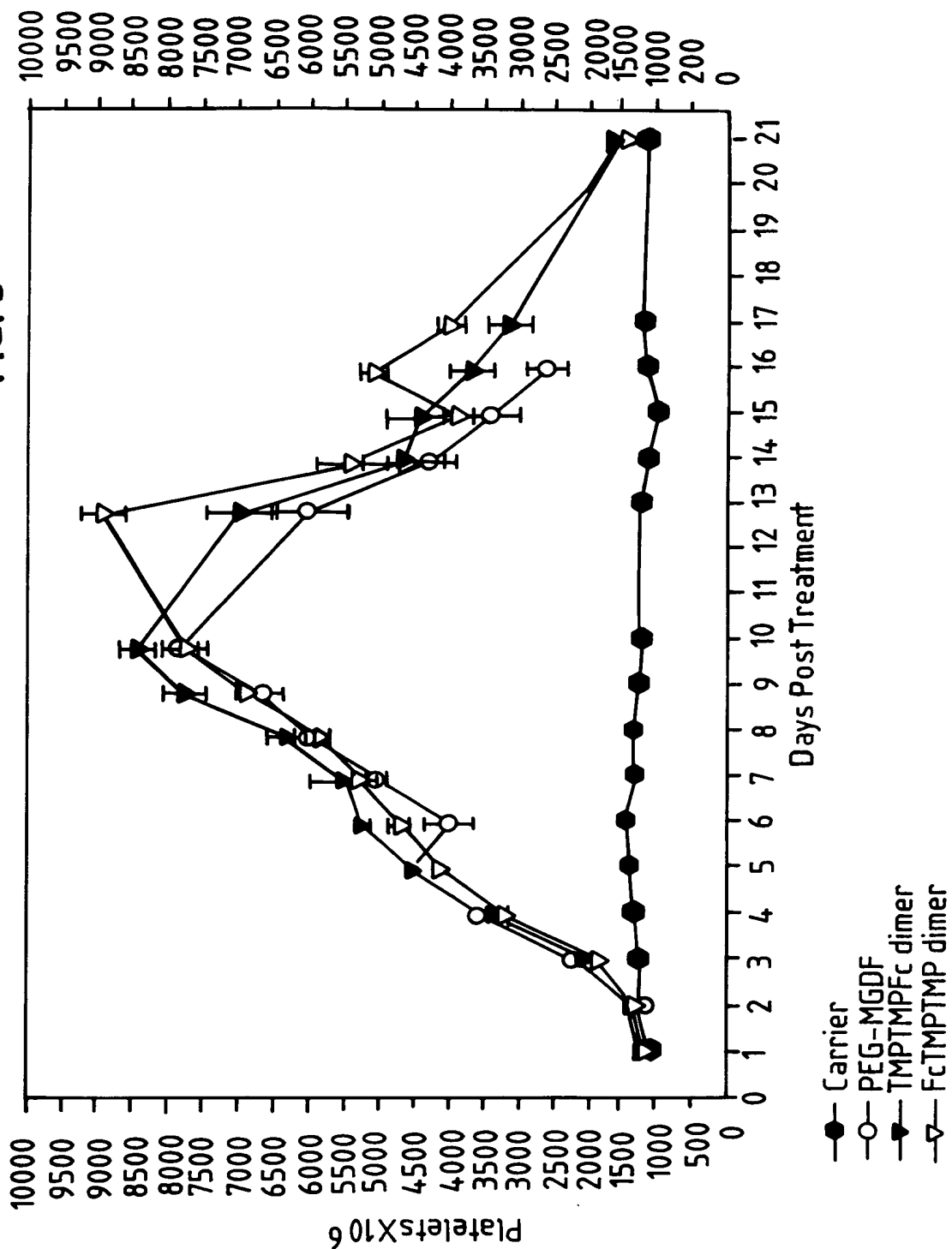




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FIG. 5





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FIG. 6A



FIG. 6B

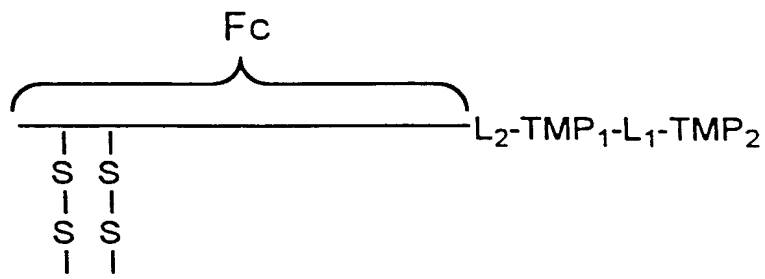


FIG. 6C

